

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 6, 2004, 19:24:00 ; Search time 66.875 Seconds
(without alignments)
43.019 Million cell updates/sec

Title: US-10-618-644-5
Perfect score: 27
Sequence: 1 TPRVF 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	48	Q41032	Q41032 pisum sativ
2	27	100.0	51	Q8QV41	Q8QV41 avian reovi
3	27	100.0	51	Q8QV42	Q8QV42 avian reovi
4	27	100.0	51	Q8QV43	Q8QV43 avian reovi
5	27	100.0	51	Q8QV46	Q8QV46 avian reovi
6	27	100.0	51	Q8QV47	Q8QV47 avian reovi
7	27	100.0	51	Q8QV48	Q8QV48 avian reovi
8	27	100.0	51	Q8QV51	Q8QV51 avian reovi
9	27	100.0	51	Q8QV52	Q8QV52 avian reovi
10	27	100.0	51	Q8QV53	Q8QV53 avian reovi
11	27	100.0	51	Q8QV55	Q8QV55 avian reovi
12	27	100.0	91	Q8QV74	Q8QV74 lactobacill
13	27	100.0	97	Q8QV75	Q8QV75 bdellovibri
14	27	100.0	97	Q8QV76	Q8QV76 bdellovibri
15	27	100.0	104	Q8QV77	Q8QV77 bdellovibri
16	27	100.0	104	Q8QV78	Q8QV78 bdellovibri
17	27	100.0	108	Q8QV79	Q8QV79 campylobact
18	27	100.0	114	Q8QV80	Q8QV80 campylobact
19	27	100.0	136	Q8QV81	Q8QV81 campylobact
20	27	100.0	138	Q8QV82	Q8QV82 campylobact
21	27	100.0	142	Q8QV83	Q8QV83 campylobact
22	27	100.0	142	Q8QV84	Q8QV84 campylobact
23	27	100.0	159	Q8QV85	Q8QV85 campylobact
24	27	100.0	167	Q8QV86	Q8QV86 campylobact
25	27	100.0	174	Q8QV87	Q8QV87 campylobact
26	27	100.0	181	Q8QV88	Q8QV88 campylobact
27	27	100.0	181	Q8QV89	Q8QV89 campylobact
28	27	100.0	188	Q8QV90	Q8QV90 campylobact
29	27	100.0	188	Q8QV91	Q8QV91 campylobact
30	27	100.0	188	Q8QV92	Q8QV92 campylobact
31	27	100.0	190	Q8QV93	Q8QV93 campylobact

32 27 100.0 193 2 Q8GBS3 Q8gb3 treponema m
33 27 100.0 195 2 Q7U656 Q7u656 synchococc
34 27 100.0 197 1 ENGB_ARCFU O28943 archaeoglob
35 27 100.0 201 2 O54257 O54257 streptomyce
36 27 100.0 205 2 O52806 O52806 amycolatops
37 27 100.0 205 2 Q939X4 Q939X4 amycolatops
38 27 100.0 206 2 Q83WF8 Q83wf8 streptomyce
39 27 100.0 207 2 Q7XTL9 Q7xtl9 oryza sativ
40 27 100.0 208 2 Q9HPH0 Q9hph0 halobacteri
41 27 100.0 237 2 Q8NLI8 Q8nli8 corynebacte
42 27 100.0 239 2 Q73M68 Q73m68 treponema d
43 27 100.0 239 2 AAS12158 Aas12158 treponema
44 27 100.0 244 1 THYX_PYRAE Q8zwd6 pyrobaculum
45 27 100.0 247 2 Q89UW7 Q89uw7 bradyrhizob

ALIGNMENTS

RESULT 1

Q41032 PRELIMINARY; PRT; 48 AA.
AC Q41032;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Legumin J (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87080257; PubMed=2431897;
RA Brown J.W.S., Feix G., Frendewey D.;
RT "Accurate in vitro splicing of two pre-mRNA plant introns in a HeLa
cell nuclear extract.";
RL EMBO J. 5:2749-2758(1986).
DR EMBL; M26771; AAA33674.1; -;
DR PIR; T06450; T06450.
FT NON TER 1
FT SEQUENCE 48 AA; 5608 MW; 0DAB5FAAF6A7B3D9 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 60; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 TPRVF 5
Db 14 TPRVF 18

RESULT 2

Q8QV41 PRELIMINARY; PRT; 51 AA.
AC Q8QV41;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL119 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL119 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354196; AAL83467.1; -;
DR InterPro; IPR007662; Reo_sigmaC.

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DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
  100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
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Db 34 TPRVF 38

RESULT 3
Q8QV42
ID Q8QV42 PRELIMINARY; PRT; 51 AA.
AC Q8QV42;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL101 80M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL101 80M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354195; AAL83466.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
  100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
   |||||
Db 34 TPRVF 38

RESULT 4
Q8QV43
ID Q8QV43 PRELIMINARY; PRT; 51 AA.
AC Q8QV43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL18 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL18 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354194; AAL83465.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
  100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
   |||||
Db 34 TPRVF 38

RESULT 5
Q8QV46
ID Q8QV46 PRELIMINARY; PRT; 51 AA.
AC Q8QV46;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL10 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL10 96M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354191; AAL83462.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
  100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
   |||||
Db 34 TPRVF 38

RESULT 6
Q8QV47
ID Q8QV47 PRELIMINARY; PRT; 51 AA.
AC Q8QV47;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL108 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177319;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL108 96M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354190; AAL83461.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
  100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
   |||||
Db 34 TPRVF 38
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RESULT 7
Q8QV48 ID Q8QV48 PRELIMINARY; PRT; 51 AA.
AC Q8QV48;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL407 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177318;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NLA07 96M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354189; AAL83460.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 8
Q8QV51 ID Q8QV51 PRELIMINARY; PRT; 51 AA.
AC Q8QV51;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEL08 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177315;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL08 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354186; AAL83457.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 9
Q8QV52 ID Q8QV52 PRELIMINARY; PRT; 51 AA.
AC Q8QV52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEL11 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEI11 97M;

DE Sigma C protein (Fragment).
OS Avian reovirus GEL07 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL07 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354185; AAL83456.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 10
Q8QV53 ID Q8QV53 PRELIMINARY; PRT; 51 AA.
AC Q8QV53;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEL04 97I.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL04 97I;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354184; AAL83455.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5632 MW; 4A0FE823ED57B1A3 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 11
Q8QV55 ID Q8QV55 PRELIMINARY; PRT; 51 AA.
AC Q8QV55;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEL11 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEI11 97M;

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RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354182; AAL83453.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0F823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 12
Q88T47 ID Q88T47 PRELIMINARY; PRT; 91 AA.
AC Q88T47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Hypothetical protein lp_3141.
GN OrderedLocNames=lp_3141.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Turchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935261; CAD65303.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 91 AA; 10638 MW; 15789F036EB55A9D CRC64;

Query Match 100.0%; Score 27; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 18 TPRVF 22

RESULT 13
Q6MNH8 ID Q6MNH8 PRELIMINARY; PRT; 97 AA.
AC Q6MNH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transglycosylase associated protein.
GN OrderedLocNames=Bdl1276;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;

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RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842649; CAE79173.1; -.
DR InterPro; IPR007341; Transglyc_assoc.
DR Pfam; PF04226; Transglyc_assoc; 1.
KW Complete proteome.
SQ SEQUENCE 97 AA; 10712 MW; F3CB159308976941 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 60 TPRVF 64

RESULT 14
CAE79173 ID CAE79173 PRELIMINARY; PRT; 97 AA.
AC CAE79173;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Transglycosylase associated protein.
GN Bdl1276.
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842649; CAE79173.1; -.
SQ SEQUENCE 97 AA; 10712 MW; F3CB159308976941 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 60 TPRVF 64

RESULT 15
Q6LHW8 ID Q6LHW8 PRELIMINARY; PRT; 104 AA.
AC Q6LHW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PPRBI240;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,

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RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378678; CAG23112.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 11783 MW; 5679626687F6916E CRC64;

Query Match 100.0%; Score 27; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
|||
Db 86 TPRVF 90

Search completed: November 6, 2004, 19:52:56
Job time : 69.875 secs

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